Phytoplankton community assessment in lake Oiskoe (Ergaki) using microscope and DNA metabarcoding

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DNA metabarcoding, namely upon the advent of next generation sequencing (NGS), has revolutionised the assessment of microbial diversity in the environment. In the case of prokaryotes, results are taken as they are, as alternative determination techniques are not comparable. In protists, a few studies have compared DNA metabarcoding to morphological microscope-based determination of taxa resulting in different protist community composition profiles according to the used technique. The double technique approach was capable to link some morphospecies with their correspondent 18S gene sequence, in a culture-free way. Nevertheless, most of the studies use either one or the other technique alone, which hampers the comparability of historical databases with current high-throughput assessments of protist diversity.

In this study, we assessed protist/phytoplankton community in lake Oiskoe (Ergaki, West Sayan) using both techniques. This survey is pioneer in two aspects: the use of DNA metabarcoding to assess environmental protist communities in the Territory of Krasnoyarsk, and the fact of sampling a mountain lake in the upper Enisey watershed in late ice-free period and early ice-covered period. Lake Oiskoe phytoplankton was dominated by Cyanobacteria in September and Bacillariophyceae in November, with a significant contribution of Chlorophyceae in both months. According to nutrient stoichiometry, Oiskoe is a nitrogen-limited lake. An impressive algal bloom (24 μg Chl x l^{-1}), mainly constituted by *Pandorina morum*, was detected in the uppermost water layer under the ice still in November, under light limiting conditions. Finally, we discuss the power of using the morphological and DNA double approach to assess protist diversity and to link the two kinds of evidence.

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